Claims:

1. A method of assessing a tissue inflammatory response comprising:

making a quantitative determination of the level of at least five transcripts shown in Table 1, or proteins encoded thereby, in a sample; and

comparing the abundance of said transcripts or proteins so determined with the level of said transcript obtained from a control sample.

2. The method according to claim 1 wherein said sample comprises cells obtained from a site within a patient believed to be affected by a tissue inflammatory response.

3. The method according to claim 2 wherein the cells are endothelial cells or said sample is of patient blood, serum or urine.

4. The method of claim 3 wherein the endothelial cells are human umbilical vein endothelial cells, human coronary artery endothelial cells or human uterine microvascular endothelial cells.

5. The method according to any one of claims 1 to 4, wherein the control sample is obtained from endothelial cells from a tissue of said patient not affected by a tissue inflammatory response.

6. The method of any one of claims 1 to 4, wherein the control sample is obtained from a tissue demonstrating an inflammatory response in said patient at an earlier point in time.

7. The method of any one of claims 1 to 6 wherein the tissue inflammatory response involves one or more of: the movement of leucocytes across an endothelium, the movement of leucocytes to inflamed tissue, the activation of leucocytes, the activation and angiogenesis of endothelial cells and/or the inhibition of apoptosis of leucocytes or endothelial cells.

8. The method according to claim 1 which is a method of diagnosing a condition with which a tissue inflammatory response is associated or monitoring the progress of a condition with which a tissue inflammatory response is associated and which is already diagnosed or monitoring the effectiveness of treatment of a condition with which a tissue inflammatory response is associated.

9. The method of any one of the preceding claims, wherein said determination is made after a course of treatment of said patient.

10. The method of any one of the preceding claims, wherein the abundance of at least 10 transcripts or proteins encoded thereby shown in Table 1 is determined.

11. The method of claim 10, wherein the abundance of at least 20 transcripts or proteins encoded thereby shown in Table 1 is determined.

12. The method of any one of the preceding claims, wherein the abundance is determined by hybridisation to a gene chip array.

13. The method of any one of claims 1-11, wherein the abundance is determined by quantitative PCR.

14. A method for the diagnosis of a condition with which a tissue inflammatory response is associated comprising the determination of the abundance of endothelial cell-derived proteins encoded by at least five of the transcripts of Table 1 in a sample from a patient suspected of suffering from such a condition.

15. The method of any of the preceding claims, wherein the tissue inflammatory response is associated with an inflammatory disease, vasculitic syndrome, atherosclerosis or an associated disease, chronic transplant rejection or wherein the condition involves tumour growth.

16. The method of claim 15 wherein the inflammatory disease includes inflammatory bowel disorders, psoriasis, ischemic reperfusion, adult respiratory distress syndrome, asthma, allergic rhinitis, dermatitis, meningitis, encephalitis, uveitis, diseases involving leucocyte diapedesis, central nervous system inflammatory disorders, Alzheimer's, endometriosis, multiple sclerosis, multiple organ injury syndrome, alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex mediated diseases; inflammation of the lung (including pleurisy, alveolitis, pneumonia, chronic bronchitis, bronchiectasis, cystic fibrosis and COPD), vasculitis, polyarteritis nodosa, giant cell arteritis, microscopic polyarteritis, pre-eclampsia and autoimmune diseases.

17. The method of any of the preceding claims, wherein said comparison determines an alteration in the pattern of

transcript levels or transcript abundance between said sample and said control sample.

18. The method of any of the preceding claims wherein the level/abundance determined is of at least one transcript or protein encoded thereby selected from: colony stimulating factor 3 (granulocyte), colony stimulating factor 2 (granulocyte-macrophage), granulocyte chemotactic protein 2, diubiquitin, ELAM-1, TNF-induced protein 6, Exodus 1, IL-1β, VCAM-1, ICAM-1, IAP1, TNF-inducible A20, RIPK2, MMP 10, TRAF1, JAK binding protein, dual specificity phosphatase 4, IL-6, IL-8, Gro-gamma, MCP-1, Gro-beta, Gro-alpha, ENA-78, fractalkine, small inducible cytokine subfamily A14, small inducible cytokine A5, LI7 receptor, toll/interleukin 1 receptor-like 4, CCAAT, MAD-3, COX-2, Mn SOD, NO synthase, L-kynurenine hydrolase, tissue factor pathway inhibitor 2, laminin gamma 2, Toll-like receptor 2, natural killer cell transcript 4, TNF-alpha induced protein 2, cationic amino acid transporter 2A, fatty acid binding protein 4, TNF receptor superfamily member 11b and TNF superfamily member 9.

19. The method of claim 18, wherein the transcript or protein encoded thereby is selected from: colony stimulating factor 3 (granulocyte), colony stimulating factor 2 (granulocyte-macrophage), granulocyte chemotactic protein 2, diubiquitin, ELAM-1, TNF-induced protein 6, Exodus 1 and IL-1β.

20. A gene chip array suitable for use in the method of any one of claims 1 to 19, comprising at least five nucleic acids suitable for detection of at least five transcripts shown in Table 1; optionally a control specific for said transcripts; and optionally at least one control for the gene chip.

21. A gene chip array for detection of at least five transcripts shown in Table 1 comprising at least five nucleic acids selected from Table 2 capable of detecting the presene of said at least five transcripts; optionally a control specific for said transcripts and optionally at least one control for said gene chip.

22. A protein based assay suitable for use in the method of any one claims 1 to 19, for the assessment of at least five proteins encoded by transcripts including those shown in Table 1, optionally a control specific for said proteins and optionally at least one control for the assay.

23. An assay according to claim 22 which is an ELISA or antibody chip.

24. An assay method for determining a modulator of a tissue inflammatory response or a condition associated therewith comprising:
a) providing a protein encoded by transcripts from Table 1;
b) bringing the protein into contact with a candidate modulator of its activity;
c) determining whether said candidate modulator is capable of modulating the activity of the protein.

25. An assay method according to claim 24, wherein said candidate modulator is an antibody or binding fragment thereof which binds said protein.

26. An assay method according to claim 24, wherein said candidate modulator is a fragment of said protein or a mimetic thereof.

27. An assay method for a modulator of a tissue inflammatory response or a condition associated therewith, wherein said method comprises
a) providing an endothelial cell in culture;
b) bringing said cell into contact with a candidate modulator of said condition; and
c) determining whether said candidate modulator is capable of modulating the level of at least one transcript of Table 1.

28. An assay method according to claim 27 wherein said candidate modulator is an antisense oligonucleotide or an RNAi.

29. An assay method according to claim 27 wherein said candidate modulator is a sense oligonucleotide.

30. Use of a modulator obtained according to the assay methods of any one of claims 24 to 29, for the treatment of a tissue inflammatory response or condition associated therewith.

31. A vector comprising a sequence encoding a transcript from Table 1b operably linked to a promoter for transcription of said sequence.

32. The vector of claim 31 wherein said sequence is linked in frame to a translation initiation region for translation of said sequence.

33. The vector of claim 31 wherein said sequence is in an antisense orientation.